

FIG. 1a

```
R  T  F  P  L  S  S  L  R  E  M  W  I  S  S  F  E  Q  S  K  458
CGG ACT CCA CCT TTG AGC TCT TTG CGA GAG ATG TGG ATT TCC AGC TTT GAA CAA TCC AAG 1376

K  E  A  Q  A  L  R  W  L  V  D  R  N  Q  N  F  S  S  Q  E  478
AAA GAA GCC CAG GCA CTA AGG TGG CTG GTT GAT AGG AAT CAA AAC TTT TCA TCT CAA GAG 1434

F  W  G  L  V  F  K  D  *  487
TTT TGG GGC CTA GTA TTC AAG GAC TGA 1461
+SEQ ID NO:37

TTTCAAAATGATCAGAATGAACAGAAAAA
```

FIG. 1b

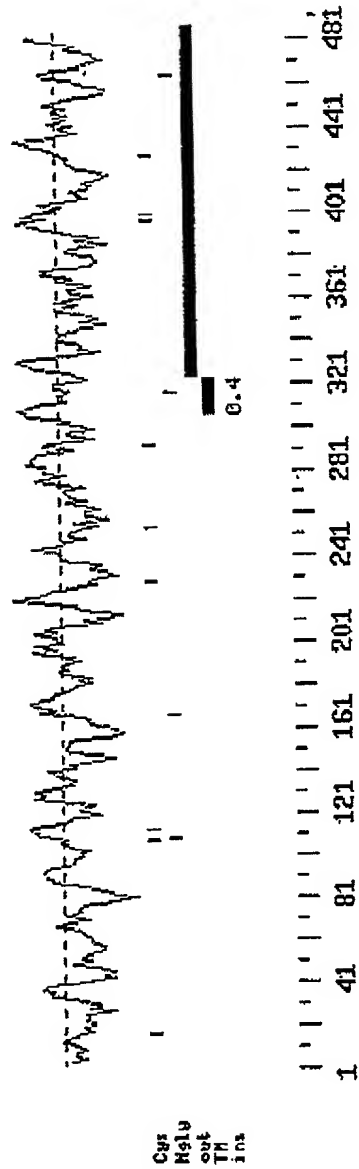


FIG. 2

```

      *->lsdafllrllwrekllGllitvppLllaiaawigleeikewkksplyL      SEQ ID NO:16
      + +  +++ ++e  + +++                +g      e +  +l
80090   35   VMVELGKFERKEF-KSSSLQ-----DGHTKMEEAP-THLN- 67

      SNDHELdVpiLlilSgapqGSrfptleenrillwtwpFndrgaPvppsrc
      + L ++ ++      r   l   +i lw+ p +  g++ + c
80090   68   -----SFLKKEGLTFNRKRKWELDSYPIMLWWSPLT--GETGRLGQC 107

      slsydntarcrltanRsel..esAdavlFNAGHhrDlsgppmdlppeft
      + + c+ t nR  l++      a lF      'D + + +l
80090  108   ----GADACFFTINRTYLhHMTKAFLF---YGTDFNIDSL-PL----- 143

      qvrarAedaDavllayednaaaaaeaLatdfpRppgQpwVwaSmESPsnsq
      pR+      w  ++ ESP n
80090  144   -----PRKAHHDWAVFHEESPKNN- 162

      RFAVPGFKiNVLNglqilldgyfNwtlSyradsDafhpYGylepltakar
      + ++      +fN t ++ + s      yle
80090  163   -----YKLFHKPVITLFNYTATFSRHSHLPLTTQYLESI----- 196

      kRGFKVqsqvVeaplnlSaKaklaAWVV...SNcntrskRerfykqLkkH
      K + + V+  +  ++ +k  A +V  +S c+  s R  ++++L
80090  197   -EVLKSLRYLVPLQS-KNKLRLKRLAPLVyvgSDCDPPSDRDSYVRELMTY 244

      lqVDvyGrv..anplplksgcsgkGve...lietlsqYkFYLaFENSqheD
      + VD yG + +  +lp  + +++      ++      +qYkF LaFEN ++ D
80090  245   IEVDSYGEClrNKDLPPQQLKNPASMDadgFYRIIAQYKFILAFENAVCDD 294

      YvTEKlWkNALqagtiPvVLgPsRavyedFvPpksFihVDDFkSakElAd
      Y+TEK+W+  l  g +Pv+ g s++      ks I V F  ++ElA+
80090  295   YITEKFWR-PLKLGVPVYYG-SPSITDWLPSNKSAILVSEFSHPRELAS 342

      YLlyLdknptAYLDmLYENPLNTLDGKAYFYQDLSFKKILDFFKTILEND
      Y++ Ld +
80090  343   YIRRLDSDDLRL----- 353

      TIYHKYseYFeWRedlrv...rlfswdalrVlEydegfCrvCrllqkapd
      Y Y eW  ++  ++rl++  lr      ++ +  d
80090  354   ----YEAYVEWKLKGEIsnqRLLTA--LR-----ERKWGVQD 384

      llelSryktiplakWFq<-*
      +++  +n+  +F+
80090  385   ----VNQ--DNYIDAFE      395
  
```

FIG. 3

Query: 89 PI-MLWNS-PLTGETGRLGQCACFFTTINRTYLHHMTKAFLFYGTDFNIDSLPLPRK 146  
P+ ++WWS ++ QCG C T R+ + LFYG++ PLPR  
Sbjct: 40 PVELVWWSRDMSWNYDVQRQCGIHTCRITNKRS--RRPWARGVLFYGSNIKTGDFPLPRN 97 SEQ ID NO:17

Query: 147 AHHDWAVPHEESPKNYKLFHKPVITLFNYTATFSRHSHLPLTTQYLESIEVLKSLRYLV 206  
H WA+ HEESP+N + +K + F++T+TFSR+S+LPLTT YL S E L S Y V  
Sbjct: 98 EHQIWALLHEESPRNTFFVSNKEFLRHFTSTFSRYSNLPLTTMYLPSGEALTSKDYV 157

Query: 207 PLQSKNKLRLAP-LVYVQSDCDPPSDRDSYVRELMTYIEVDSYGECLRNKDLPOQLKN 265  
K+K R + +V++QSDCD S R+ YV+EIM ++ +DSYG CLRN+DLP++ K+  
Sbjct: 158 TFDGSKYGYRPTSTSVVFLQSDCDTMSGREYVKELMKHLPIDSYGSLRNRLDPERQKD 217

FIG. 4

Query: 221 LVYVQSDCDPPSDRDSYVRELMTYIEVDSYGECLRNKDLPOQLKNPASMDADGFYRIIAQ 280  
+ +V S+ +P S R Y ++L +++VD YG R K LPQ +++  
Sbjct: 62 VAWVVSNNPNSARVRYYYQLQKHLKVDVYGRSHRGKPLPQ-----GNMMETLSR 111 SEQ ID NO:18

Query: 281 YKFILAFENAVCDDYITEKFWR-PLKLGVPVYVYGPSITDW---LPSNKSAILVSEFSH 336  
YKF LAFEN++ DYITEK WR L+ G VPV G PS ++ +P + + I V +F  
Sbjct: 112 YKFYLAFENSMHPDYITEKLWRNALEAGAVPVVLG-PSRVNYERFIPPD-AFIVDDFQS 169

Query: 337 PRELASYIRRLSDDRLYEAYVEWKLKGEIS 367  
P+ELA Y++ LD + Y Y+ WK + ++  
Sbjct: 170 PKELAKYLKELDKNHAAYLKYLRLWKYENPLN 200

FIG. 5

Query: 90 IMLWWSPLTGETGRLGQCCADACFFTINRTYLHHMTKAF--LFYGTD--FNIDSLPLPR 145  
I+LW P +CG C T +R+ H KAF + D ++ + L  
Sbjct: 129 ILLWNEPSLVNAPAHVECG---CLVTTSRS---HNDKAFDAVVISADHPYSFEGLG-GV 180 SEQ ID  
NO:19

Query: 146 KAHHD-WAVPHEESPKWNYKLFHKPV--ITL--FNYTATFSRHSPLPLTTQYLESIEVLK 200  
K H D +AV+ + P ++ + P+ TL FN T T+ S L T Y + +  
Sbjct: 181 KLHPDFYAVYAAKKPLSSTQ--NPLTNFTLPPFNLTMTYRLDSQLIWTDYFSSHNLAR 237

Query: 201 SLRYLVPLQSKNKLRLAPLVY-VQSDCDPPSDRDSYVRELMTYIEVDSYGECLRNKDL 259  
L++ SK+ A V ++S+ S L Y+ + + L  
Sbjct: 238 RLKWF-RAPSKSFADDMPTTVLRLESEILKKS-----RLAVYLVYEVNEKTLPEPLY 289

Query: 260 PQQLKNPASMADA-DGFYRIIAQYKFI LAFENAVCDDYITEKFWRPLKLGVPVYVYGSPLI 318  
++L+ A +DA D Y F+L FE + C DY+ + + +VPV G ++  
Sbjct: 290 MEELRKYADLDAHDNCLGTDHDFMLIFETSACPDYVPPQMSMAMDKLLVPVVLIGGGNL 349

Query: 319 TDWLPSNKSAILVSEFSPRELASYIRRLDSDRLYEAYVEW---KLKGEISNQRLLTA 374  
T+ +PS+ S I +F+ P++L +++ L ++ Y Y W +L+ L +  
Sbjct: 350 TNLVPSH-SYISSQDFATPQDLIIHLKDLANNQLEYRRYFWWHYSIYRLRKTSPYCALCS 408

Query: 375 LRERKNGVQDVNQDNY 390  
L ++ G +V Q +Y  
Sbjct: 409 LIQQSPGGHEVRQRSY 424

FIG. 6

AGCTGCCCTTTGCAGACTCTAACTCCAGCAGC	H N V S F A H L H F A G	12	SEQ ID NO:5
ATG AAT GTG TCC TTT GCT CAC CTC CAC TTT GCC GGA		36	SEQ ID NO:4
↑SEQ ID NO: 6→			
G Y L P S D S Q D W R T I I P A L L V A		32	
GGG TAC CTG CCC TCT GAT TCC CAG GAC TGG AGA ACC ATC ATC CCG GCT CTC TTG GTG GCT		96	
V C L V G F V G N L C V I G I L L H N A		52	
GTG TGC CTG GTG GGC TTC GTG GGA AAC CTG TGT GTG ATT GGC ATC CTC CTC CAC AAT CCT		156	
W K G K P S M I H S L Y L N L S L A D L		72	
TGG AAA GGA AAG CCA TCC ATG ATC CAC TCC CTG ATT CTG AAT CTC AGC CTG GCT GAT CTC		216	
S L L L F S A P I R A T A Y S K S V W D		92	
TCC CTC CTG CTG TTT TCT GCA CCT ATC CGA GCT ACG GCG TAC TCC AAA AGT GTT TGG GAT		276	
L G W F V C K S S D W F I H T C M A A K		112	
CTA GGC TGG TTT GTG TGC AAG TCC TCT GAC TGG TTT ATC CAC ACA TGC AGG GCA GCC AAG		336	
S L T I V V V A K V C F H Y A S D P A K		132	
AGC CTG ACA ATC GTT GTG GTG GCC AAA GTA TGC TTC ATG TAT GCA AGT GAC CCA GCC AAG		396	
Q V S I H N Y T I W S V L V A I W T V A		152	
CAA GTG AGT ATC CAC AAC TAC ACC ATC TGG TCA GTG CTG GTG GCC ATC TGG ACT GTG GCT		456	
S L L P L P E W F F S T I R H H E G V E		172	
AGC CTG TTA CCC CTG CCC GAA TGG TTC TTT AGC ACC ATC AGG CAT CAT GAA GGT GTG GAA		516	
M C L V D V P A V A E E F M S H F G K L		192	
ATG TGC CTC GTG GAT GTA CCA GCT GTG GCT GAA GAG TTT ATG TCG ATG TTT GGT AAG CTC		576	
Y P L L A F G L P L F F A S F Y F W R A		212	
TAC CCA CTC CTG GCA TTT GGC CTT CCA TTA TTT TTT GCC AGC TTT TAT TTC TGG AGA GCT		636	
Y D Q C K K R G T K T Q N L R N Q I R S		232	
TAT GAC CAA TGT AAA AAA CCA GGA ACT AAG ACT CAA AAT CTT AGA AAC CAG ATA CGC TCA		696	
K Q V T V M L L S I A I I S A L L W L P		252	
AAG CAA GTC ACA GTG ATG CTG CTG AGC ATT GCC ATC ATC TCT GCT CTC TTG TGG CTC CCC		756	
E W V A W L W V W H L K A A G P A P P Q		272	
GAA TGG GTA CCT TGG CTG TGG GTA TGG CAT CTG AAG GCT GCA GGC CCG GCC CCA CCA CAA		816	
G F I A L S Q V L M F S I S S A N P L I		292	
GGT TTC ATA GGC CTG TCT CAA GTC TTG ATG TTT TCC ATC TCT TCA GCA AAT CCT CTC ATT		876	
F L V M S E E F R E G L K G V W K W H I		312	
TTT CTT GTG ATG TCG GAA GAG TTC AGG GAA GGC TTG AAA GGT GTA TGG AAA TGG ATG ATA		936	
T K K P P T V S E S Q E T P A G N S E G		332	
ACC AAA AAA CCT CCA ACT GTC TCA GAG TCT CAG GAA ACA CCA GCT GGC AAC TCA GAG GGT		996	
L P D K V P S P E S P A S I P E K E K P		352	
CTT CCT GAC AAG GTC CCA TCT CCA GAA TCC CCA GCA TCC ATA CCA GAA AAA GAG AAA CCC		1056	
S S P S S G K G K T E K A E I P I L P D		372	
AGC TCT CCC TCC TCT GGC AAA GGG AAA ACT GAG AAG GCA GAG ATT CCC ATC CTT CCT GAC		1116	
V E Q F W H E R D T V P S V Q L K S T N		392	
GTA GAG CAG TTT TGG CAT GAG AGG GAC ACA GTC CCT TCT GTA CAA TTG AAG AGC ACC AAC		1176	
P T D C G S S G N S A W Y R K T E K S A		412	
CCT ACA GAT TGT GGT AGC TCA CGT AAC TCA GCG TCG TAC CGC AAA ACT GAA AAA TCA GCA		1236	
C C P K T E I H S T F Y F Q I L L L A Y		432	
TGT TGC CCT AAG ACG GAA ATC CAT TCA ACA TTC TAC TTC CAG ATA CTG CTT CTA GCA ATT		1296	
H R N R N H I S R F S T K Q L L L G L Q		452	
CAC AGA AAC AGA AAC CAC ATC TCA CGT TTC TCA ACT AAA CAA CTG CTT TTA GGA CTG CAG		1356	

FIG. 7a

462  
1306

[illegible]

FIG. 7b





```

*->GNILVilviltkklr..tptnifilNLavADLLfilitlppwalyyl  seq ID NO:20
GNl Vi ++l +      +++++ + +ilNL++ADL +ll+  p+  +++++
52874   40  GNLCVIGILLHNWKGKpSMIHSLILNLSLADLSLLLFSAPIRATAY 86

vggsedWpfGsalCklvtaldvvnmyaSillLtaIS<-*
+ W +G ++Ck +  ++ ++m a l++++ +
52874   87  SK--SVWDLGWfVCKSSDWFihTCMAAKSLTIVVVA      120

```

FIG. 9a

```

*->kvvillvWvlallslPpllfswvktveegngtlnvntvClidfpe  seq ID NO:21
+ v++++W++a ll lP +fs+ +++e+ +      +Cl+d p
52874   142  WSVLVAIWTVASLLPLPEWFFSTIRHHEGVE-----MCLVDVPA 180

estasvstwlrsyvllstlvGFlilPlilvYtrilrtlr.....
++      +++++ + l l++F lPl++ +++ +r +      +++++++
52874   181  VA---EEFMSMFGKLYPLLAfGLPLFFASfYFWRAYDQCKKrgtktgnl 226

.....kaaktllvvvvvFvICWlPyfivllldtlc.lsiimsstCele
+++ +++++ +ll + ++ +l+WlP +++l+ ++ + +
52874   227  rmgirskQVTVMLLSIAIISALLWLPWVAVLWVWHLKAAGP----- 268

rvlptallvtlwLayvNsciNPiIY<-*
+ ++ ++ ++ +L ++ S' NP+I
52874   269  APPQGFIALSQVLMFSSISANPLIF      293

```

FIG 9b

```

Query:  253  EWVAVLW-VWHLKAAGPAPPQGFIALSQVLMFSSISANPLIFLVMSEEFREGLKGVW--- 308
        EW  WL+ V+H      F +S VL +  S+ NP+++ +MS FRE K V
sbjct:  12  EWTEWLYDVYHY-----FHMVSGVLfYLLSSAINPILYNLMShRFREAPKNVLSSL 61  seq ID NO:22

Query:  309  --KWMITKKP-PTVS 320
        +W      KP P+ S
sbjct:  62  CKQWHSRHKPRPSFS 76

```

FIG. 10

Query: 208 YFWRAYDQC-KKRGTKTQNLNRNQIRSKQVTVMXXXXXXXXXXXXXWLPBWVAWLWVWHLKAA 266  
YF C +KR +T+ + R+ +VT+M WLP W+ W ++A  
Sbjct: 160 YFKIILKMCQRKQMOTKRTATKRTTKVTIMGLAIVISYTHCWLPPFWIVQ---WSIEAN 216 SEQ ID NO:23  
Query: 267 GPAPPQGFIALSQVLMFSI----SSANPLIFLVMSEEFREGLKGVWKMWITKKP 316  
+ + F++ S+ANP +++ +S+ F+ K + K + T KP  
Sbjct: 217 LFEKSKYLLFCCTHFAPALQYINSAANPFLYVFLSDSFQ---KNIQKLLRTAKP 267

FIG. 11

Query: 16 PSDSQDWR--TIIPALL---VAVCLVGFVGNLCVIGILLHNAWKGPSPMI-HXXXXXXXXX 69  
PSD+ + T++ +L + L+ F N+ + G++ W K +++ H  
Sbjct: 115 PSDAPETYSDTVLSVVLGFYALLLLIAFASNILLAGVIKKYRWGMKQALLFHLCTGALL 174 SEQ ID NO:24  
Query: 70 XXXXXXXXXAP----IRATAYSKSVWDLGNFVCKSSDWFHTCMAAKSLTIVVVAKVCF- 124  
A ++ S +V L F + W H A + ++ +A CF  
Sbjct: 175 SITNTLHLLASGYHLLKQRNSSTV--LQSFALIA--WVDHFIGFALLIFVMYLAIFCFK 230  
Query: 125 MYASDPKQVSI-HNYTIWSVLVAIWTVASLLPLPEWFFSTIRHHEGVEMCLVDVPAVAE 183  
Y ++ + + +Y +++V ++ W +A L+ PF H + C+ V AV+  
Sbjct: 231 FYWNNKTRSIENGRSYVLYAV-ISTWVIAFLIAGFTAFFQCDSHINSQDQCIQIVCAVSN 289  
Query: 184 EFMSMFGKL 192  
F ++F +L  
Sbjct: 290 IFSAIFTEL 298

FIG. 12

TACTCACTATAGGGCTCGAGCGGCCGCCCGGGCAGGTCTAGAAATTCAGCGGCCGCTGAATTTCTAGGCTGCTCTGGGCTT SEQ ID NO:7  
TGCTAGCCGGCTCTGCACCTCCAGAGCCGTTGGGCACGCCCTCAGCTGCTCCATCGCCTCACTTTCCAGGCTCGCG

CCCGAAGCAGAGCCATGAGAACCCCGGGTGCCTGGCGAGCCGCTAGCGCC M G F G E A L 7 SEQ ID NO:8  
↑SEQ ID NO: 9↓ ATG GGC CCG GGC GAG GCG CTG 21

L A G L L V H V L A V A L L S N A L V L 27  
CTG GCG GGT CTT CTG CTG ATG GTA CTG GCC GTG-GCG CTG CTA TCC AAC GCA CTG GTG CTG 81

L C C A Y S A E L R T R A S G V L L V N 47  
CTT TGT TGC GCC TAC AGC GCT GAG CTC CGT ACT CGA GGC TCA GGC GTC CTC CTG GTG AAT 141

L S L G H L L L A A L D M P F T L L G V 67  
CTG TCG CTG GGC CAC CTG CTG CTG GCG GCG CTG GAC ATG CCC TTC ACG CTG CTC GGT GTG 201

M R G R T P S A P G A C Q V I G F L D T 87  
ATG CGC GGG CGG ACA CCG TCG GCG CCC GGC GCA TGC CAA GTC ATT GGC TTC CTG GAC ACC 261

F L A S N A A L S V A A L S A D Q W L A 107  
TTC CTG GCG TCC AAC CCG GCG CTG AGC GTG GCG GCG CTG AGC GCA GAC CAG TGG CTG GCA 321

V G F P L R Y A G R L R P R Y A G L L L 127  
GTG GGC TTC CCA CTG CGC TAC GCC GGA CGC CTG CGA CCG CGC TAT GCC GGC CTG CTG CTG 381

G C A W G Q S L A F S G A A L G C S W L 147  
GGC TGT GCC TGG GGA CAG TCG CTG GCC TTC TCA GGC GCT GCA CTT GGC TGC TCG TGG CTT 441

G Y S S A F A S C S L R L P P E P E R P 167  
GGC TAC AGC AGC GCC TTC GCG TCC TGT TCG CTG CGC CTG CCG CCC GAG CCT GAG CGT CCG 501

R F A A F T A T L H A V G F V L P L A V 187  
CGC TTC GCA GCC TTC ACC GCC ACG CTC CAT GCC GTG GGC TTC GTG CTG CCG CTG GCG GTG 561

L C L T S L Q V H R V A R S H C Q R H D 207  
CTC TGC CTC ACC TCG CTC CAG GTG CAC CGG GTG GCA CGC AGC CAC TGC CAG CGC ATG GAC 621

T V T M K A L A L L A D L H P S V R Q R 227  
ACT GTC ACC ATG AAG GCG CTC GCG CTG CTC GCC GAC CTG CAC CCC AGT GTG CGG CAG CGC 681

C L I Q Q K R R R H R A T R K I G I A I 247  
TGC CTC ATC CAG CAG AAG CGG CGC CGC CAC CGC GCC ACC AGG AAG ATT GGC ATT GCT ATT 741

A T F L I C F A P Y V M T R L A E L V P 267  
GCG ACC TTC CTC ATC TGC TTT GCC CCG TAT GTC ATG ACC AGG CTG GCG GAG CTC GTG CCC 801

F V T V N A Q W G I L S K C L T Y S X A 287  
TTC GTC ACC GTG AAC GCC CAG TGG GGC ATC CTC AGC AAG TGC CTG ACC TAC AGC AAG GCG 861

V A D F F T Y S L L R R P F R Q V L A G 307  
GTG GCC GAC CCG TTC ACG TAC TCT CTG CTC CGC CGG CCG TTC CGC CAA GTC CTG GCC GGC 921

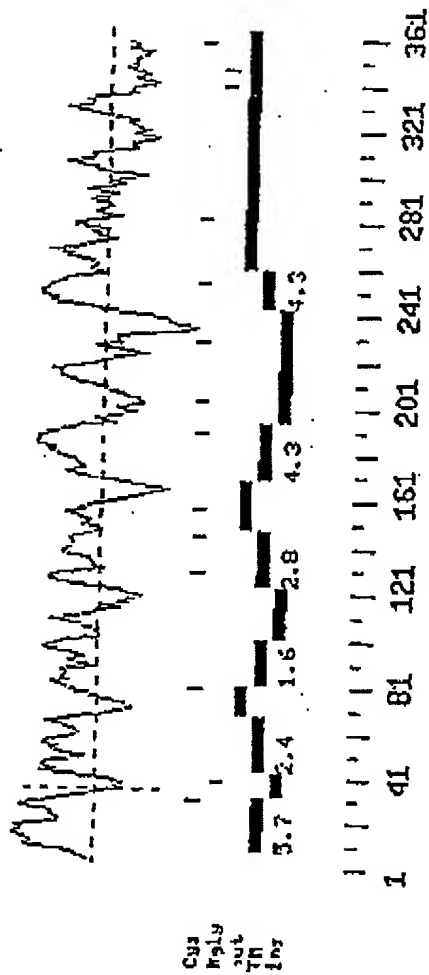
M V H R L L X R T P R P A S T H D S S L 327  
ATG GTG CAC CGG CTG CTG AAG AGA ACC CCG CGC CCA GCA TCC ACC CAT GAC AGC TCT CTG 981

D V A G H V H Q L L K R T P R P A S T H 347  
GAT GTG GCC GGC ATG GTG CAC CAG CTG CTG AAG AGA ACC CCG CGC CCA GCG TCC ACC CAC 1041

N G S V D T E N D S C L Q Q T H \* 364  
AAC GGC TCT GTG GAC ACA GAG AAT GAT TCC TGC CTG CAG CAG ACA CAC TGA 1092

GGGCCTGGCAGGGCTCATCGCCCCACCTTCTAAGAAGCCCTGTGGAAGA <SEQ ID NO:9T

FIG. 13



**FIG. 14**

```

*->GNILVilvilrtkklr.tptnifilNLAVADLLflltclppwaiylylv  SEQ ID NO:25
      N+LV+l  +++  lr++++  ++++NL++  LL++++  +p+l+  ++
52880  22  SNALVLLCCAYSABLRTASGVLLVNLSLGHLLLAALDMFPFTLLGVM 68

      ggsdWpfGsalCklvtaldvnmYaSillLtaISiDRYlAlvhPlryrr
      g  + p  +  C  +  ++ld++  1+  aa+S D +iA+  Plry
52880  69  RG--RTPSAPGACQVIGFLDTFLASNAALSVAALSADQWLAVGFPLRYAG 116

      rrtsprrAkvvillvWvlallslPpllfswvktveegngtlnvntvCl
      r  +  pr A  ++++++W  +l++s  l++++  ++  +C+
52880  117  RLR-PRYAGLLLGCAWGQSLAFSGAA-LGCSWLGYS--FASCS 157

      idfpeestasvstwlrsyvlstlvGFlPllvilvcYtrilrtlr....
      +  p  e+  ++  +++  ++  vgF+lPl  v++  +  +++  r++r++  +
52880  158  LRLPPEP---ERPRFAAFTATLHAVGFVLPLAVLCLTSLQVHRVARshcq 204

      .....kaaktllvvvvFvlCW
      +  ++  +  +  +  +++  +++  +++++++a++  +++  +  +F++C+
52880  205  rmdtvtmkalalladlhpsvrqrcliqgkrrrhRATRKIGIAIATFLICF 254

      lpyfiVllldtlc.lsiimsetCelervlptallvtlWlayvNscINPiI
      +Py  +  l  +  v  +  +++  +L+y+  ++  +P+
52880  255  APYVMTRLAELVPFVT-----VNAQWGILSKCLTYSKAVADPFT 293

      Y<-*
      Y
52880  294 Y  294

```

FIG. 15

```

Query:  134  SLAFSGAALGCSWLGYSFAFASCSXXXXXXXXXXXXFAAFTATLHAVGFVLPLAVLCLTSL 193
      +L F  AL  SWLG+  +ASC+  FA FT+  HA+  F+L  VLC T L
Sbjct:  2  ALTFPATALALSWLGFHQLYASCTLCSSRPDERLRFVFTSAFHLSFLLSFIVLCFTYL 61  SEQ ID NO:26

Query:  194  QVHRVARSHCQMDTVMKALALLADLHPSVRQRCLIQKRRRHRRATRKIGIAIATFLIC 253
      +V  +VAR  HC+R+D  +TM+  L  LL  D+HPSVR+RCL  +QKRRR  RAT+KI  I  TFL+C
Sbjct:  62  KVLKVARFHCKRIDVITMOTLVLLVDIHPSVRERCLEEQKRRRQRATKKISTFIGTFLVC 121

Query:  254  FAPYVMTRLAELVPFVTVNAQWGILSKCLTYSKAVADPFTYSLRRPFRQVLGMVHRL 313
      FAPYV+TRL  EL  +++  WG+LSKCL  YSKA  +DPF  YSLLR  +R+  +++R+
Sbjct:  122  FAPYVITRLVELFSTAPIDSHWGLSKCLAYSKAASDPFVYSILLRHQYRRSCKELNRI 181

Query:  314  KR 315
      R
Sbjct:  182  NR 183

```

FIG. 16

Query: 175 TLHAVGFVLPLAVL--CLTS--LQVHRVARSHCQRMDTVMTKALALLADLHPSVRQRC LI 230  
TL VGF++P V+ C L VH + + D + A +  
Sbjct: 28 TLFIIVGFMIPCLVIIVCYACIFLTVHH-QKKKIRNHDNFQIAAAKGSSSSGGGSYMTTTC 86 SEQ ID NO:27

Query: 231 QQKRRRHRATRK-IGIAIATFLICFAPY---VMTRLAELVPFVTVNAQ---WGILSKCL 282  
+K R R T K + + F IC+ P V+ R+ + N W I S L  
Sbjct: 87 TRKAREDRKTTKMLMVVFLCFAICYLPISILNVLKRVEGFMFRHSEDNESVYVWHIFSHWL 146

Query: 283 TYSKAVADPFTYSLLRRPFRQVLAGMVHRLKRTTPR PAS 321  
Y+ + +P Y+ + +R+ + LLK P S  
Sbjct: 147 VYANSCINPIIYNFMNGKYRKAY-WKIFALLKFWGEPLS 184

FIG. 17

Query: 171 AFTATLHAVGFVLPLAVL-----CLTSLQVHRVARSHCQRMDTVMTKALALLADLHPSVR 225  
A+ L F +P +V+ C+ + H R H D++ + ++ L L R  
Sbjct: 24 AYVVMLEVVAVFFIFBSVMLYSYMCILNTVRHNAVRIH-NHPDSLCLSQVSKLG-IMSLQR 81 SEQ ID NO:28

Query: 226 QRCLIQKRRRHRATRKIGIAIATFLICFAPY-VMTRLAELVPFVTVNAQWGILSKC--- 281  
+ + RA I I F +C+ P+ V + L+ + +S C  
Sbjct: 82 PHQMSVDMSEKTRAFTTILILFVGFSLCWLPHSVSYLSVFSKHFFYQHNFFEISTCVLW 141

Query: 282 LTYSKAVADPFTYSLLRRPFRQVLAGMVHRLKRTTPR-PAST 322  
L Y K+V +P Y + FR+ M+ + K P+ P T  
Sbjct: 142 LCYLKSVFNPIIYCWRIKKFREACLEMPKTFKILPQVPGRT 183

FIG. 18

Query: 221 HPSVRQRC LIQQKRRRHRATRKIGIAIATFLICFAPYVMTRLAELVPFVTVNAQWGILSK 280  
H ++ CL+QQKR+ A+ G+A A +P R F W L  
Sbjct: 7 HKIIKAACLVQQKREQFLASVARGVAPAD-----SPEAPRR-----SFAGGTWDWEYLQ- 55 SEQ ID NO:29

Query: 281 CLTYSKAVADPFTYSLLRRPFRQVLAGMVHRLKRTTPR PASTHDSLDV 329  
+ A+ F Y RR RQ G VH LL P P +S+LD+  
Sbjct: 56 -FASPEEYAE-FQY---RRRHRQRRRGDVHSLLSNPPDPDEPSESTLDI 99

FIG. 19

CTGTGACTTTAAGTATTTCTAAGGCGCAGAGCAATGGGAGGTGGAGAACTGCTGGGTTGCAGGTGACACTATAACGTAGA SEQ ID NO:10

TCATGCCTCCTATTTCCATGCAGGACCTCCAGCCCTGAAGCAACATCAGTGACAGACATCACTGGCAGA H 1 SEQ ID NO:11  
ATG 3  
↑SEQ ID NO:12→

A S R Y V A V G M I L S Q T V V G V L G 21  
GCC TCC CGG TAT GTG GCA GTG GGA ATG ATC TTA TCA CAG ACC GTG GTG GGA GTC CTG GGG 63

S F S V L L H Y L S F Y C T G C R L R S 41  
AGC TTC TCT GTT CTT CTC CAT TAT CTC TCC TTT TAC TGC ACT GGG TGC AGG TTA AGG TCC 123

T D L I V K H L I V A N F L A L R C K G 61  
ACA GAT TTG ATT GTT AAG CAC CTG ATT GTA GCC AAC TTC TTA GCT CTC CGC TGT AAA GGA 183

V P Q T M A A F G V R Y F L N A L G C K 81  
GTC CCC CAG ACA ATG GCA GCT TTT GGG GTT AGA TAT TTT CTC AAT GCT CTT GGG TGC AAA 243

L V F Y L H R V G R G V S I G T T C L L 101  
CTT GTT TTC TAT CTC CAT AGA GTG GGC AGG GGA GTG TCC ATT GGC ACC ACC TGC CTC TTG 303

S V P Q V I T V S S R K S R W A K L K E 121  
AGT GTC TTC CAG GTG ATC ACG GTC AGC TCC AGG AAA TCC AGG TGG GCA AAA CTT AAA GAG 363

K A P K H V G F S V L L C W I V C M L V 141  
AAA GCC CCC AAG CAT GTT GGC TTT TCT GTT CTC CTG TGC TGG ATC GTG TGC ATG TTG GTA 423

N I I F P K Y V A G K W N Y T N I T V N 161  
AAC ATC ATC TTT CCC ATG TAT GTG GCT GGC AAA TGG AAC TAC ACA AAC ATC ACA GTG AAC 483

E D L G Y C S G G G N N K I A Q T L R A 181  
GAG GAT TTG GGA TAC TGT TCT GGG GGA GGC AAC AAC AAA ATC GCA CAG ACA CTG CGT GCA 543

M L L S F P D V L C L G L M F W V S S S 201  
ATG TTG TTA TCA TTC CCT GAT GTG TTG TGT CTG GGG CTC ATG TTC TGG GTC AGC AGC TCC 603

M V C I L H R H K Q R V Q H I D R S D L 221  
ATG GAT TGC ATA CTG CAC AGG CAC AAG CAG CGG GTC CAG CAC ATT GAT AGG AGC GAT CTC 663

S P R A S P E H R A T Q S I L I L V S T 241  
TCC CCC AGA GCC TCC CCA GAG AAC AGA GCT ACG CAG AGC ATC CTC ATC CTG GTG AGC ACC 723

F V S S Y T L S C L F Q V C M A L L D N 261  
TTT GTG TCT TCT TAC ACT CTC TCC TGC CTT TTC CAA GTT TGT ATG GCT CTT TTG GAT AAT 783

P N S L L V N T S A L M S V C F F T L S 281  
CCC AAT AGT TTA CTG GTG AAC ACT TCA GCC TTA ATG AGT GTA TGT TTC CCA ACT CTC AGC 843

P F V L H S C D F S V Y R F C F A W K R 301  
CCC TTT GTT CTC ATG AGC TGT GAC CCC AGT GTA TAC AGG TTT TGT TTT GCC TGG AAA AGA 903

TGA 302  
←SEQ ID NO:12↑ 906

CAAGATCTCCTAACCTCATATAACATGTACATTGTATATATTTCCTCATGGTTCAATTGATGACTTACTCTTCTGTG

CCGCACCTGCCCCGGGCGGCGCTCGAGCCCTATAGTGAGTA

FIG. 20



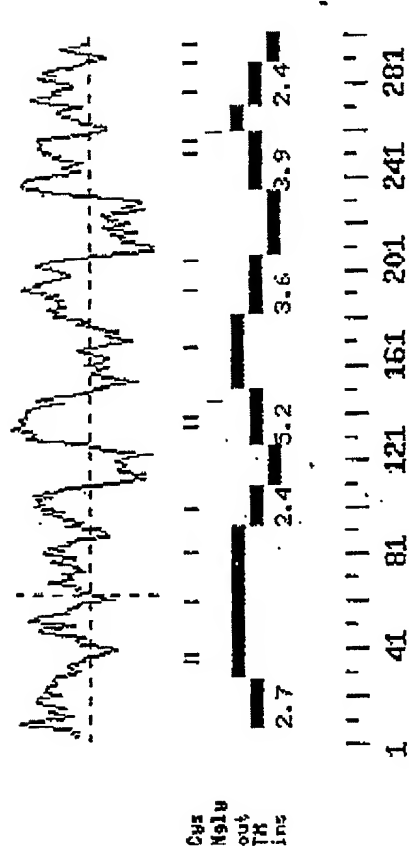


FIG. 21

```

-->llPlilvilvcYtrIltlr.....kaaktl SEQ ID NO:30
+i+l ++ + + ++++l+++++ ++ ++++ +++ +++++a+ +
63497 189 VLCLGLMFVSSSMVCILHrhkqrqhidsdlspaspenRATQSI 235

lvvvvfv<-*
l++v++fv
63497 236 LILVSTFV 243

```

FIG. 22

```

Query: 36 GCRLRSTDLIVKHLIVANFLALRCKGVPTMAAFGVRYFLNALGCKLVFYLHEVGRGVSI 95
      G R R TDL + L + + + L G TM F + CK + YLHR+ RG+S+
Sbjct: 5 GERSRPTDLPIGLLSLVFLMMLLTMGFIATMDMFMSWGRWDDTCKSLIYLHRLLRGLSL 64 SEQ ID NO:31

Query: 96 GTICLLSVFQVITVSSRSRMAKLKEKAPKHVGFSVLLCWIVCMVNIIPPMYVAGKWNV 155
      TTCLL+VFQ IT+S R S AK K K+P H+ + L W++ M + + + N
Sbjct: 65 CTICLLNVFOAITLSFRSSCLAKFKHKSPHHSCTFLFLWVLYMSFSSEHLLLSIATPNL 124

Query: 156 TNITVNEDLGYSGGGNNKLAQTLRAMLLSFDPVLCGLGMFWSSSMVCILHrhkqrqh 215
      T+ CS + Q++ + LL+ DV +GLM S MV +L RH+++ QH
Sbjct: 125 TSNDFMYVTQSCSILPMSYSMSMFSTLLAIROVFLIGLMVLSSGYMVALLCPHRKQAQH 184

Query: 216 IDRSDLSPRASPENRATQSILILVSTF-VSSYTL-SCLFQVCMALLDNFNSLLVNTSALM 273
      + + LSP+ASPE KAT++IL+L+S+F V Y S +F D P + ++
Sbjct: 185 LHSTSLSPKASPEQPATRITLMLMSSFFVLMYIFDSIVFCSRTMFKDGPTFYCIQI--IV 242

Query: 274 SVCFPTLSPFVLMSCDPSVYRF 295
      S + T+SPFV + + + +F
Sbjct: 243 SHSYATVSPFVFICTEXHIVKF 264

```

FIG. 23

TGCCAGGGGAGACAGGAACCTCTTCCCTTCTCTGTGTGTCAGGATCGCAGAAAGTATGTCCCTTCTCTCACC																			
																			K
																			ATG
																			↑Seq ID No: 15→
S	W	L	S	S	S	Q	G	V	V	L	T	A	Y	H	P	S	G	K	D
AGC	TGG	CTC	TCC	AGT	TCC	CAG	GGA	GTG	GTA	CTA	ACA	GCC	TAC	CAC	CCC	AGC	GGC	AAG	GAC
Q	A	V	G	N	S	F	A	K	A	G	E	E	A	T	S	S	R	R	Y
CAG	GCC	GTC	GGG	AAC	AGC	CAT	GCA	AAG	GCA	GGG	GAG	GAA	GCC	ACC	TCG	AGT	CGC	AGA	TAT
G	Q	Y	T	M	N	Q	E	S	T	T	I	K	V	M	E	K	P	P	F
GGC	CAG	TAC	ACT	ATG	AAC	CAG	GAA	AGC	ACC	ACC	ATC	AAA	GTT	ATG	GAG	AAG	CCT	CCA	TTT
D	R	S	I	S	Q	D	S	L	D	E	L	S	M	E	D	Y	W	I	E
GAT	CGA	TCA	ATT	TCC	CAG	GAT	TCT	TTG	GAT	GAA	CTA	TCT	ATG	GAA	GAC	TAT	TGG	ATA	GAA
L	E	N	I	K	K	S	S	E	N	S	Q	E	D	Q	E	V	V	V	V
CTA	GAA	AAC	ATC	AAG	AAA	TCT	AGT	GAA	AAC	AGC	CAA	GAA	GAT	CAA	GAG	GTG	GTT	GTT	GTC
K	E	P	D	E	G	E	L	E	E	E	W	L	K	E	A	G	L	S	N
AAA	GAG	CCT	GAT	GAG	GGA	GAA	TTG	GAA	GAA	GAG	TGG	CTT	AAA	GAG	GCC	GGT	TTA	TCC	AAT
L	F	G	E	S	A	G	D	P	Q	E	S	I	V	F	L	S	T	L	T
CTC	TTC	GGA	GAG	TCT	GCT	GGA	GAT	CCA	CAG	GAA	AGC	ATT	GTG	TTT	TTA	TCA	ACA	TTG	ACG
P	T	Q	A	A	A	V	Q	K	R	V	E	T	V	S	Q	T	L	R	K
CGG	ACC	CAG	GCA	GCA	GCA	GTT	CAG	AAG	CGA	GTA	GAG	ACG	GTC	TCC	CAG	ACC	TTG	AGA	AAA
K	N	K	Q	Y	Q	I	P	D	V	R	D	I	F	A	Q	Q	R	E	S
AAA	AAC	AAA	CAG	TAC	CAG	ATT	CCT	GAC	GTC	AGA	GAC	ATA	TTT	GCT	CAA	CAG	AGA	GAA	TCA
K	E	T	A	P	G	G	T	E	S	Q	S	L	R	T	N	E	N	K	Y
AAA	GAA	ACA	GCT	CCA	GGT	GGC	ACT	GAA	TGG	CAG	TCA	CTT	AGA	ACA	AAT	GAA	AAC	AAA	TAC
Q	G	R	D	D	E	A	S	N	L	V	G	B	E	K	L	I	P	F	E
CAA	GGA	AGA	GAT	GAC	GAG	GCA	TCT	AAC	CTT	GTT	GGT	GAA	GAG	AAG	CTG	ATC	CCA	CCT	GAG
E	T	P	A	P	E	T	D	I	N	L	E	V	S	F	A	E	Q	A	L
GAG	ACG	CCT	GCC	CCT	GAA	ACA	GAC	ATC	AAC	CTG	CAG	GTA	TCA	TTT	GCC	GAG	CAA	GCA	CTC
N	Q	K	E	S	S	K	E	K	I	Q	K	S	K	G	D	D	A	T	L
AAT	CAG	AAA	GAG	AGC	TCC	AAG	GAG	AAA	ATC	CAG	AAG	AGC	AAA	GTC	GAT	GAT	GCC	ACA	TTA
P	S	F	R	L	P	K	D	K	T	G	T	T	R	I	G	D	L	A	P
CCT	AGT	TTC	AGA	TTG	CCA	AAA	GAC	AAA	ACG	GGT	ACC	ACA	AGG	ATT	GGT	GAC	CTC	GCA	CCC
Q	D	M	K	K	V	C	H	L	A	L	I	E	L	T	A	L	Y	D	V
CAG	GAC	ATG	AAG	AAA	GTT	TGC	CAT	TTA	GCC	CTA	ATT	GAG	CTG	ACT	GCC	CTC	TAT	GAT	GTA
L	G	I	E	L	K	Q	Q	K	A	V	K	I	K	T	K	D	S	G	L
TTG	GGT	ATT	GAG	CTG	AAA	CAA	CAA	AAA	CCT	GTG	AAA	ATC	AAA	ACA	AAA	GAT	TCT	GGT	CTT
F	C	V	P	L	T	A	L	L	E	Q	D	Q	R	K	V	P	G	H	R
TTT	TGC	GTT	CCA	TTG	ACA	GCG	CTA	TTA	GAA	CAA	GAT	CAG	AGG	AAA	GTA	CCA	GGA	ATG	CCA
I	P	L	I	F	Q	K	L	I	S	R	I	E	E	R	G	L	E	T	E
ATA	CCC	TTG	ATC	TTT	CAA	AAA	CTG	ATT	TCT	CGA	ATT	GAA	GAG	AGA	GGT	TTG	GAA	ACA	GAA
G	L	L	R	I	P	G	A	A	I	R	I	K	N	L	C	Q	E	L	E
GGC	CTC	TTA	CGG	ATC	CCT	GGA	GCT	GCC	ATT	AGA	ATC	AAG	AAT	CTT	TGC	CAA	GAA	CTA	GAA
A	K	F	Y	E	G	T	F	N	W	E	S	V	K	Q	H	D	A	A	S
GCA	AAG	TTT	TAT	GAA	GGG	ACT	TTT	AAT	TGG	GAA	AGT	GTC	AAA	CAG	CAT	CAT	GCC	GCC	AGC
L	L	K	L	F	I	R	E	L	P	Q	P	L	L	S	V	E	Y	L	K
CTG	CTG	AAG	CTC	TTC	ATT	CGG	CAG	TTG	CCC	CAG	CCA	CTC	CTC	AGT	GTG	GAG	TAT	CTC	AAA
A	P	Q	A	V	Q	N	L	P	T	K	K	Q	Q	L	Q	A	L	N	L
GCC	TTT	CAG	GCT	GTC	CAG	AAT	CTT	CCA	ACC	AAG	AAG	CAG	CAA	CTA	CAG	GCT	TTG	AAC	CTT

FIG. 24a

L V I L L P D A N R D T L K A L L E F L	461
CTT GTC ATC CTC CTA CCT GAT GCA AAC AGG GAC ACA CTG AAG GCC CTT CTT GAA TTT CTC	1383
Q R V I D N K E K N K M T V M N V A M V	481
CAA AGA GTA ATA GAT AAT AAA GAA AAA AAT AAA ATG ACA GTC ATG AAT GTA GCA ATG GTC	1443
M A P N L F M C H A L G L K S S E Q R E	501
ATG GCC CCG AAT CTC TTT ATG TGT CAT GCA TTG GGA TTG AAG TCC AGT GZA CAG CGA GAA	1503
F V M A A C T A N T M H L L I K Y Q K L	521
TTT GTA ATG GCA GCT GGG ACA GCA AAT ACC ATG CAC TTA TTG ATT AAG TAC CAA AAA CTT	1563
L W T I F K F I V N Q V R K Q N T E N H	541
CTG TGG ACA ATT CCC AAG TTT ATT GTA AAC CAA GTG AGG AAG CAA AAC ACG GAA AAT CAT	1623
K K D K R A M K K L L K K M A Y D R E K	561
AAA AAG GAT AAA AGA GCC ATG AAG AAA TTG CTG AAG AAA ATG GCT TAT GAC CGA GAA AAA	1683
Y E K Q D K S T N D A D V P Q G V I R V	581
TAT GAA AAG CAA GAT AAG AGT ACA AAT GAT GCT GAC GTT CCT CAG GGA GTG ATT CGA GTG	1743
Q A P H L S K V S M A I Q L T E E L K A	601
CAA GCT CCC CAT CTT TCG AAA GTT TCC ATG GCA ATA CAG CTA ACT GAA GAA CTA AAA GCC	1803
S D V L A R F L S Q E S G V A Q T L K K	621
AGT GAT GZA CTT GCC AAG TTT CTC AGC CAA GAA AGT GGG GTT GCC CAG ACT CTC AAG AAA	1863
G E V F L Y E I G G N I G E R C L D D D	641
GGA GAA GTT TTT TTG TAT GAA ATT GGA GGA AAT ATT GGG GAA CGC TGC CTT GAT GAT GAC	1923
T Y M K D L Y Q L N F N A E W V I K S K	661
ACT TAC ATG AAG GAT TTA TAT CAG CTT AAC CCA AAT GCT GAG TGG GTT ATA AAG TCA AAG	1983
P L *	664
CCA TTG TAG	1992
←SEQ ID NO:15 ↑	
AAGACTTAACAGCTGTCAGATAACCATGTGGACTTCTGTCTAATAATCTTGCTGAGTCAGAGTGTAAATAAAGAAATG	
GCAGGACATATATTATTCAGTTGTACCCAAAGTATTTAAAAATGACTCTCTTTAAGCCTTAAAGGTCATAGATTGTGCT	
GCTGCCAGAAATATATTAATTATTTAATGTTATTTATAGAAAAAAATTTCTGGAGTGAAGATAAAGAGGCTTAAT	
AGTTTGTGGCCAGSTTTTCATATGCTCTGTGAATGTGTCCAGATGTGCATAGTTCTTTTATTTTAAATATGTGGAATG	
TCTTCTCTCCCATTCITTTCTCTTAAATCATATATAGTGTAAATATATGCTCTCTCAGCTCTATTACCTCTCCACATC	
TACCCITTTCCCASTTAGGTTTGCTTTTGGACCAAAAGATAGCAAAATACCAGGTATGGCAAGTTGTGAAGACAGGCAT	
TAAACATACCTAAATTTCACAGTATTCCTGTCCAGCAGAGAATGTTAGTATTTCATCTCTTTGAAATCATTTGCTCAAAAT	
TAACTTCCACCTTTTCTGTCTATCAACGGAAGTGATTGCAATTTTCTTCAGTTTCATCTGACTTATGTTCAACAGAA	
CCGTATCAGCGACCAAGAAAATAGGACTGTGAGAAGCTGCCAGTTATTTACTGAACCATTAATATCTATATACTAAGAA	
TAAATAAAAATATACCCATGTGAATAATAATTTGGATTATGGATAACAGAGAGTGAAGGCCAAGCACTTTCTGTCTAC	
TGTACTCTTCAAAATGGAATTTTAAAGTCATAGCTGGCTTTACGTGTGTCTATTATAGCATTATAAATATGCATGAT	
AGTATAATCCAGTAATGGTTGAAGAAATGATTTTAACTTAAAGAGGGATTTTTTTTTTTAAGTCCGAAATAAGTCTACTG	
GAAGAATTAATCTCTCGGGTGAAAAAGCTTTGTGTGTGTCTTATTTTAAATAAACCGGAGTCAATTTATTAATGTT	
CTTGAAGTACTATTCCAGGGATTTTATATGCACAAACCATATTGTGACAAAGAGATGAGCCCTCTGTACTGTAATAAGA	
AATGAAGTAGAGAAATGTTAAATATTTATGAGCTTTACAAATATAGTAAATAAAAGGTCATGTAAATGAATGCTGCACAA	
ACGSGTGTTCATGATACTTTTAGTAGTACTTTAGGAAAACTACACATTCTCAGAAGCTCTTGATGTCTCTAATGAAGGG	
GGGGAATGCTGTAAATGAGAACAGTCATAAAATTTTACCATATAATTAACAAGACAGCCTGTGGATATGATCACTTAA	
TGATTTTCTGGTGATTCTGTGCCATTGCTTTTTTATTTAAAGAAAAATTTGTAAATTAATGCCCTTTTCTAAAAAAA	

FIG. 24b

AAAAA

[illegible]

**FIG. 24c**

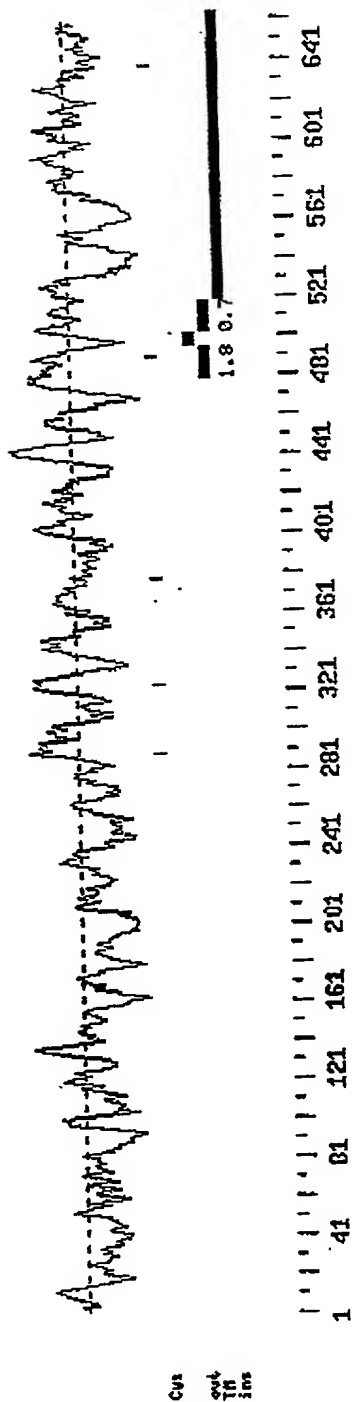


FIG. 25

```

*->PifivekcveyleklyPLaerGlqeEGiYRvsGsa...srvkeLrea SEQ ID NO:32
P+i +k+++ Ie+ rGl++EG+ R++G a + +++++eL ++
33425 343 PLIFQKLISRIEE-----RGLTEGLLRIPGAAirikNLCQELEAK 383

fdkdgapdslelsekewfdvhvvgllKlYlReLPePLipydlyeefira
f ++ + + e+ ++ h a+lLkL++ReLP+PL++ + + f
33425 384 FYEG--TFNWESVKQ-----HDAASLLKLFIRELPQPLLSVEYLKAFQAV 426

akeqiedpderiralkellsSkLPrahynTLryLltHlnrvaeiyiensa
+ ++ ++l+al+ l+ +LR+a+++Tl++Ll++L+rv+ n +
33425 427 QN--LPTKKQQLQALNLLVI--LLPDANRDTLKALLEFLQRVID---NKE 469

vNkMnarNLaiVfgPtLlrppdkesnd<-*
+NKM++ N A v +P+L+ + ++
33425 470 KNKMTVMNVAMVMAPNLFMCHA--LGL 494

```

FIG. 26

```

Query: 516 IKYQKLLWTIPKFIVNQVRKQNTENHXXXXXX--XXXXXXXXXXYDREK-----YEKQ 565
+KYQK+LW +P F++ QVR+ N +RE +K
Sbjct: 1 LKYQKILWKVPSFLITQVRMNEATMLLKROLPSVRKLLRRKTLERETASPKTSKVLQKS 60 SEQ ID NO:33

Query: 566 DKSTNDADVPOGVIRVQAPHL SKVSMAIQLTEELKASDVLARF 608
+ +DVP+GVIRV AP LSKVSMAIQL + KA D+LA+F
Sbjct: 61 PSARMSDVPEGVIRVHAPLLSKVSMAIQLNNQTKAKDILAKF 103

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FIG. 27

```

Query: 390 NWESVKQ-HDAASLLKLFIRELPQPLLSVE----YLKAFQA-VQNLPTKXXXXXXXXXX 443
N E + H A LLK + RELP+PLL+ E +++A +A V + +
Sbjct: 16 NMEEYEDVHTVAGLLKQYFRELPEPLLTLYEYEEFIEAQAQVSDERMEALEMLKELI 75 SEQ ID NO:34

Query: 444 XXXPDANRDTLKALLEFLQRVIDNKEKNKMTVMNVAMVMAPNL 486
P+ANR+TL+ LL+ L RV + E+NKM N+A+V P l
Sbjct: 76 KLLPEANRETLYLLKHLRVAQHSEENKMNAQNLAUVFGPTL 118

```

FIG. 28

Query: 399 AASLLKLFIRELPQPLLSVBYLKAFQAVQNLPKKXXXXXXXXXXXXXXXXPDANRDTLKALL 458  
A SLLKLF+REL P+PLL+ + + F+ V + P P NR L +L  
Sbjct: 96 ACSLLKLFRLRELPEPLLTDLVARFEEVASHPKVTTQQAELQQLLEQLPKNRTLLAWVL 155 SEQ ID NO:35

Query: 459 EFLQRVIDNKEKNKMTVMNVAMVMAFNLFM 488  
VI + NK+ ++AM+++P L M  
Sbjct: 156 LHFDAVIOQERHNKLNQSLAMLLSEPTLQM 185

FIG. 29